

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 21:52:24 ; Search time 71.96 Seconds
(without alignments)
259,843 Million cell updates/sec

Title: US-09-456-306-2

Peptide score: 2965
Sequence: 1 MAISYAEQLIDTLEAGVKR.....GGVGAMIDLANSIRINRITP 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1317.5	44.1	572	1	POXB_ECOLI
2	902.5	30.2	396	1	Y142_PSEAY
3	586.5	19.6	591	1	ILVW_METJA
4	560	18.8	603	1	POXB_LACPL
5	554.5	18.6	573	1	ILVW_BACSU
6	533.5	17.9	575	1	ILVW_GUTH
7	533.5	17.9	590	1	ILVW_PORPU
8	536	17.6	618	1	ILVW_MYCTU
9	523.5	17.5	562	1	ILVW_ECOLI
10	517.5	17.3	579	1	ILVW_ECOLI
11	507	17.0	548	1	ILVW_ECOLI
12	503	16.9	625	1	ILVW_MYCLE
13	493	16.5	670	1	ILVW_ARATH
14	482	16.5	591	1	POXB_STRPN
15	480	16.1	655	1	ILVW_KLEPN
16	477	16.0	652	1	ILV3_BRANA
17	464.5	15.6	621	1	ILVW_MYCAV
18	461	15.4	626	1	ILVW_CORGL
19	454	15.2	664	1	ILV2_TOBAC
20	454	15.2	667	1	ILV1_TOBAC
21	449	15.0	575	1	ILVW_LACLA
22	441.5	14.8	637	1	ILV2_BRANA
23	442	14.1	559	1	ILVW_KLETE
24	430	14.1	574	1	ILV1_ECOLI
25	418.5	14.0	669	1	ILVW_SCHPO
26	414	13.9	687	1	ILVW_YEAST
27	393	13.2	559	1	ILVW_KLEPN
28	390.5	13.1	573	1	ILV1_HAEIN
29	385.5	12.9	571	1	ILV1_BUCAP
30	356	11.9	592	1	GCL_ECOLI
31	332	11.1	494	1	Y663_METJA
32	316.5	10.6	540	1	ILVW_BACSU
33	313	10.5	547	1	ILVW_MYCTU

RESULT ID	POXB_ECOLI	STANDARD:	PRT: 572 AA.
AC	P07003: Q47513; Q47514; Q47515; Q47516; Q47517; Q47518; Q47519; Q47520;		
AD	01-APR-1988 (Rel. 07, Created)		
DT	01-APR-1988 (Rel. 07, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	PYRUVATE DEHYDROGENASE [CYTOCHROME] (EC 1.2.2.2) (PYRUVATE OXIDASE)		
DE	(POX) (PYRUVATE DEHYDROGENASE [UBIQUINONE]).		
GN	POXB		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
OC	Escherichia.		
RC	[1]		
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RC	STRAIN-K12:		
RX	MEDLINE-86286555; PubMed-3016647;		
RA	Grabau C., Cronan J.E., Jr.;		
RT	"Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate oxidase, a lipid-activated flavoprotein.";		
RL	Nucleic Acids Res. 14:5449-5460(1986).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-K12 / MG1655;		
RX	MEDLINE-97426617; PubMed-9278503;		
RA	Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;		
RT	"The complete genome sequence of Escherichia coli K-12.";		
RL	Science 277:1453-1474(1997).		
RC	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-K12:		
RX	MEDLINE-97061202; PubMed-8905232;		
RA	Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kikugawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N., Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiiuchi T.;		
RT	"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";		
RL	DNA Res. 3:137-155(1996).		
RN	[4]		
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.		
RC	STRAIN-K12:		
RX	MEDLINE-89308683; PubMed-2663858;		
RA	Grabau C., Chang Y.Y., Cronan J.E., Jr.;		
RT	"Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small alterations of the carboxyl-terminal region.";		
RL	J. Biol. Chem. 264:12510-12519(1989).		
RN	[5]		
RP	SEQUENCE OF 550-572 FROM N.A.		
RC	MEDLINE-86033917; PubMed-3902830;		

ALIGNMENTS

34	287.5	9.6	563	1	B2NB_PSEFL	P51853 pseudomonas
35	282.5	9.5	564	1	OXE_ECOLI	P78093 escherichia
36	274.5	9.2	580	1	IOID_BACSU	P42415 bacillus su
37	271	9.1	528	1	MDIC_PSEPU	P20906 pseudomonas
38	257	8.6	560	1	YECO_YEAST	P39994 saccharomyc
39	238	8.0	545	1	DCIP_AZOBR	P51852 azospirillum
40	222	7.4	568	1	OXE_OXAFO	P40149 oxalobacter
41	215	7.2	571	1	DCPI_SCHPO	P09737 schizosacch
42	196	6.6	552	1	DCIP_ENTML	P23234 enterobacte
43	186.5	6.2	568	1	DCPY_ZYMMO	P06672 zymomonas m
44	174	5.8	563	1	DCPI_KIULA	O12629 kluyveromyc
45	174	5.8	570	1	DCPY_NEUCR	P33287 neurospora

RA Recny M.A., Grabau C., Cronan J.E., Jr., Hager L.P.:
 RT "Characterization of the alpha-peptide released upon protease
 RL activation of pyruvate oxidase."
 RL J. Biol. Chem. 260:14287-14291(1985).
 [6]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=94293772; PubMed=8022274;
 RA Chang Y.Y., Wang A.Y., Cronan J.E., Jr.:
 RT "Expression of Escherichia coli pyruvate oxidase (PoxB) depends on
 RL the sigma factor encoded by the ipos(katf) gene."
 RL Mol. Microbiol. 11:1019-1028(1994).
 CC -1- CATALYTIC ACTIVITY: PYRUVATE + FERRICYTOCHROME B1 + H(2)O = CO(2)
 CC + ACETATE + FERROCYTOCHROME B1.
 CC -1- COFACTOR: THIAMINE PYRROPHOSPHATE, FAD AND MAGNESIUM ION.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 CC -1- PTM: ACTIVATED BY LIMITED PROTEOLYTIC DIGESTION. THIS CLEAVAGE
 CC PRODUCES A PEPTIDE (ALPHA-PEPTIDE) AND MIMICS THE ACTIVATION OF
 CC ENZYME BY PHOSPHOLIPIDS. THE PROTEOLYTIC CLEAVAGE ALSO RESULTS IN
 CC THE LOSS OF THE HIGH AFFINITY LIPID-BINDING SITE OF THE ENZYME.
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
 CC -----
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 CC -----
 DR EMBL: X04105; CAA27725.1; -
 DR EMBL: AE000188; AAC73958.1; -
 DR EMBL: D90724; BAA35585.1; -
 DR EMBL: S73268; AAB31180.1; -
 DR EMBL: M28208; AAB59101.1; -
 DR EMBL: L47688; AAB59102.1; -
 DR EMBL: L47689; AAB59103.1; -
 DR EMBL: L47690; AAB59104.1; -
 DR EMBL: L47691; AAB59105.1; -
 DR EMBL: L47692; AAB59106.1; -
 DR EMBL: L47693; AAB59107.1; -
 DR EMBL: L47694; AAB59108.1; -
 DR EMBL: L47695; AAB59109.1; -
 DR PIR: A23648; DEECPC.
 DR HSSP: P37063; 1POM.
 DR SWISS-2DPAGE: P07003; COLI.
 DR ECODBASE: G058.0; 6TH EDITION.
 DR ECGENE: B610754; POXB.
 DR INTERPRO: IPR000399; -
 DR PFAM: PF00205; TPP_ENZYMES; 1.
 DR PROSITE: PS00187; TPP_ENZYMES; 1.
 DR Oxidoreductase; Flavoprotein; FAD; Thiamine pyrophosphate; Magnesium;
 KW Membrane; Lipid-binding.
 KM
 FT PEPTIDE 550 572
 FT ACT_SITE 50 50 ALPHA-PEPTIDE.
 FT MUTAGEN 533 533 BY SIMILARITY.
 FT MUTAGEN 553 553 A->T: IN POXB11.
 FT MUTAGEN 560 560 A->V: IN POXB14.
 FT MUTAGEN 564 564 D->P: IN POXB15; NORMAL ACTIVITY.
 FT MUTAGEN 572 572 R->G: IN POXB16; LOSS OF ACTIVITY.
 FT INTERACT LESS WITH MEMBRANES.
 FT MUTAGEN 549 572 MISSING: IN POXB6.
 FT MUTAGEN 564 572 MISSING: IN POXB7.
 FT MUTAGEN 570 572 MISSING: IN POXB8.
 FT CONFLICT 364 365 OO -> HE (IN REF. 4).
 FT CONFLICT 414 416 OAL -> HGV (IN REF. 4).
 FT SEQUENCE 572 AA; 62011 MW; 57B38B9E3A92BDEA CRC64;

Query Match 44.1%; Score 1317.5; DB 1; Length 572;
 Best Local Similarity 46.3%; Pred. No. 3.7e-79;
 Matches 266; Conservative 106; Mismatches 195; Indels 7; Gaps 6;

OY 1 MAHSVAEQLIDTLEAGQVKRIYGLVDSLNPIYDAV-ROSDIEWVHVNEEAAFAAGAE 59
 Db 1 MKQVAAVIAKLTLESAGVKRWGVTGDSLNKSLRMGMETEMSTRHEEVAFAAGAE 60
 OY 60 SLITGELAVCAASCGPGNTHLIGLYSHRNKAVLAIAHSIPSAQIGSFPEQTHEIL 119
 Db 61 AQLGELAVCAGSCGPGNHLINGLFPCRHRNVVLAIAAHIPSELSGSGFQDTHOEL 120
 OY 120 FKESGCEWNGGEGGERILNHAIGSMAGKGVSVVYIPDIDKEPDAGDYSNSTISS 179
 Db 121 FRESHCELVSSPEQLPVYLAIMKRAVLNRGVSYYVLPEVDALAKRAPEGA-TMHYTHA 179
 OY 180 GTPVFPDPTEAALVLEANNKSVTLFCGAVKNARQVLEAEIKSPIGALGKQY 239
 Db 180 PQPVTPPEELRLKLAQLRYSSNIALMGSCAGAHKELEFAGIKAPIVHALRKEH 239
 OY 240 IOHENPEFVGSGLGYACADSNADLLILDTDFPYSFLPKD-NVNOVDINGHIG 298
 Db 240 VEYDNPVYVGTGLIGFSSGPHTMNADTLVLTQTPPYRAFPYDPAKITQIDINPASTIG 299
 OY 299 RRTVYKYPVTDVATINILPHYEKTRSFILDMKAHERKLSVVEYTHNVEKHP 358
 Db 300 AHSKYDALVGDIKSTLRALLPIYEKADRKFDKALEDY-RDARKGLDLAKSEK--A 356
 OY 359 IHPEVVASILNELADKDAVFTVDMCNVHARYIENEGTRDVGSRFCTANALPHA 418
 Db 357 IHPYLAQOISHEAADDITFCDDVGTPTVMAARYLK-MNGKRRLIGSFNHSNANMFOA 415
 OY 419 IGAQSVDRNRVIMCGGGGMLGELLTYKHLQPLKAVFNNSISGWKLEMLEGQ 478
 Db 416 LGAQTEPEROVAMCGGSGSMLMGDFLSVQMKLPKIVYFNNSVIGFAAMEKAGY 475
 OY 479 PEFGTDEHEVFAELTAAAGIKSVARITDPKRVQDLAEALAPGVLIDITDPNALISIP 538
 Db 476 LTDGELHDTNPARIAECGITGIRKEKASEVDEALQAFSIDPVLVDVVAKEELAIIP 535
 OY 539 PLTIWEQWGFSGSKATRVFPGGVAMTDLARSN 572
 Db 536 POKLEQAKGFSLYMLRAIISGRGDEVIELAKTN 569
 RESULT 2
 Y142_PSEAY STANDARD: PRT; 396 AA.
 AC P10343;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE HYPOTHETICAL 42.6 KDA PROTEIN IN ISOMYLASE 3' REGION.
 OS Pseudomonas amyloclavata.
 OC Bacteria; Proteobacteria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SB-15;
 RA Amezura A., Fujita M., Futai M.;
 Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: SIMILAR TO E. COLI ACETOHYDROXY ACID SYNTHASE.
 CC -----
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 CC -----
 DR EMBL: X13378; CAA31755.1; -
 DR PIR: S01682; S01682.
 DR HSSP: P37063; 1POM.
 DR INTERPRO: IPR000399; -
 DR PFAM: PF00205; TPP_ENZYMES; 1.
 KW Hypothetical protein.
 SEQUENCE 396 AA; 42613 MW; EBAC54942050B03B CRC64;

"The refined structures of a stabilized mutant and of wild-type pyruvate oxidase from *Lactobacillus plantarum*."; J. Mol. Biol. 237:315-335(1994). [2]

RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=93174262; PubMed=8438155;
 RA Muller Y.A., Schulz G.E.;
 RT "Structure of the thiamine- and flavin-dependent enzyme pyruvate oxidase.";
 RL Science 259:965-967(1993).

CC -!- FUNCTION: IMPORTANT FOR THE AEROBIC GROWTH. DECARBOXYLATES PYRUVATE IN FOUR STEPS. THE ENERGY RELEASED IS PARTIALLY STORED IN ACETYL PHOSPHATE.
 CC -!- CATALYTIC ACTIVITY: PYRUVATE + O(2) + H(2)O = ACETYL PHOSPHATE + CO(2) + H(2)O(2).
 CC -!- COFACTOR: THIAMINE PYRROPHOSPHATE, FAD AND MAGNESIUM ION.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- DOMAIN: EACH MONOMER IS DIVIDED INTO THREE DOMAINS, EACH OF WHICH CONTAINS A SIX-STRANDED PARALLEL BETA SHEET SURROUNDED BY ALPHA HELICES.
 CC -!- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
 CC PDB: 1POW; 31-JAN-94.
 DR PDB: 1POX; 31-JAN-94.
 DR INTERPRO: IPR000399; -.
 DR PFM: PF00205; TPP_ENZYMES; 1.
 DR PROSITE: PS00187; TPP_ENZYMES; 1.
 KM Oxidoreductase; Flavo-protein; FAD; Thiamine pyrophosphate; Magnesium; 3D-structure.
 FT DOMAIN 1 191
 FT DOMAIN 192 342
 FT DOMAIN 343 603
 FT ACT_SITE 59 59
 FT METAL 447 447
 FT METAL 474 474
 FT METAL 476 476
 FT STRAND 10 12
 FT STRAND 13 23
 FT STRAND 24 25
 FT STRAND 28 31
 FT STRAND 35 46
 FT HELIX 47 50
 FT STRAND 52 55
 FT STRAND 59 73
 FT STRAND 77 81
 FT STRAND 83 84
 FT TURN 85 88
 FT TURN 89 90
 FT TURN 91 99
 FT HELIX 100 101
 FT STRAND 104 110
 FT STRAND 113 117
 FT TURN 121 122
 FT TURN 127 130
 FT HELIX 131 133
 FT TURN 136 139
 FT STRAND 144 145
 FT TURN 146 160
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 FT TURN 163 169
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 FT STRAND 176 178
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 FT TURN 186 188
 FT STRAND 196 196
 FT STRAND 199 211
 FT STRAND 215 219
 FT HELIX 221 237
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 FT HELIX 326 336
 FT HELIX 344 364
 FT TURN 365 365
 FT STRAND 370 370
 FT HELIX 373 383
 FT TURN 386 387
 FT STRAND 389 392
 FT HELIX 396 404
 FT TURN 409 410
 FT STRAND 412 414
 FT TURN 422 423
 FT HELIX 425 435
 FT STRAND 437 438
 FT TURN 441 446
 FT HELIX 447 462
 FT TURN 463 464
 FT STRAND 468 473
 FT STRAND 476 476
 FT STRAND 478 487
 FT HELIX 496 496
 FT STRAND 502 509
 FT TURN 510 510
 FT STRAND 512 516
 FT STRAND 518 518
 FT HELIX 519 532
 FT TURN 533 535
 FT STRAND 538 543
 FT TURN 552 553
 FT TURN 559 561
 FT HELIX 564 574
 FT TURN 575 575
 FT TURN 577 578
 FT HELIX 582 588
 FT TURN 589 590
 SQ SEQUENCE 603 AA; 66141 MW; 71BEC3CF52060FBE CRC64;

Query Match 18.8%; Score 560; DB 1; Length 603;
 Best Local Similarity 27.5%; Pred. No. 1.8e-29;
 Matches 147; Conservative 116; Mismatches 251; Indels 20; Gaps 8;

QY 9 LIDTLEAGVGRKRTYGLVGLSDLPIDAV--ROSDIEWVHVRNEEAAAFAGAESTLTGEL 66
 Db 17 VIKVLEAMGVBDHLYGLPGSINSIMDALSAERDRHYIYVRHEFGAMAAADAKLTCKI 76
 QY 67 AVCAASCGPGNTHLIQGLVDSHRNGAKYLAIALSHIPSAQIGSTFFQETHPELFEKCSGY 126
 Db 77 GVCFGSAGPGGTHLMNGILDAREDHVPVLAALIGQGTGMNMDTFQEMMENPIYADVADY 136
 QY 127 CEMVNGEGEGERLHHAISTVMAKGVSYVYIPGDIKADADDGTYNSNTISSGTPV-F 185
 Db 137 NVTAVNAATLPVHIDEAIRAVAHOGVAVVQIPVDLPWQOIPAEPMVYASANSYQTPLEP 196
 QY 186 PDPTAAALVEAIIINNAKSYTLFCGAGVKNARAQVLEAEIKSPIGHALGCKQYIOHENP 245
 Db 197 PDVQAVTRLITQILLAEERLIYIGIGARKAGKLEDLSTKLIPLMSTYPAKGIYADRP 256
 QY 246 FEVMSGLIGYACVDASNEADLLILGTFEYS---FLPKDNVAQYDINGAHIIGRT 301
 Db 257 AYLGSANRYAKQRPANALAOADVLFVGNYPFAEVSFAKNTRYFLQIDIDPAKLGKHH 316
 QY 302 YKVPYPTGVAAATIEMLIPHVKEKTDRLDMML---KAHEKLISSVVEITYHNNEKNRP 358
 Db 317 KTDIAVLADAKRTLAAILLAQVSESTPWWQANLANVKNMRAVYLASTLED-----KQEGP 370

CC Eukaryota: Cryptophyta; Cryptomonadaceae; Guillardia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99128221; PubMed=9929392;
 RA Douglas S.E., Penny S.L.;
 RT "The plastid genome of the cryptophyte alga, Guillardia theta:
 complete sequence and conserved syntenic groups confirm its common
 ancestry with red algae.";
 RL J. Mol. Evol. 48:236-244(1999).
 CC -1- CATALYTIC ACTIVITY: 2-ACETOYLACTATE + CO(2) = 2-PYRUVATE.
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION
 CC (BY SIMILARITY).
 CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
 CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY).
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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 CC -----
 DR EMBL: AF041468; AAC35740.1; -
 DR INTERPRO: IPR000399; -
 DR PFAM: PF00205; TPP_ENZYMES; 1.
 DR PROSITE: PS00187; TPP_ENZYMES; 1.
 KW branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;
 KM Thiamine pyrophosphate; Lyase; Chloroplast.
 FT ACT SITE 60 BY SIMILARITY.
 SQ SEQUENCE 575 AA: 63359 MW: F9447P9A178D3EC4 CRC64;

Query Match 17.9%; Score 533.5; DB 1; Length 575;
 Best Local Similarity 28.0%; Pred. No. 9,1e-28;
 Matches 161; Conservative 114; Mismatches 251; Indels 49; Gaps 17;

QY 9 LIDTLEAGVKKRYGLVGSUNPIYDAV-----RQSDIEVHVRNEAFAAGASGLING 64
 DB 16 LIDSLVRHCVKKEIFEGYGGALIPYDELAYAMEKEGFTIEHLVNRHGGASHASDGAARSTG 75
 QY 65 ELAVCAASGPGNTHLIOGLYDSHRNGAKVLAISHIPSAOIGSTPFQEE-----THPEI 118
 DB 76 NVCVCATSGPKNLTIVTGATAMHDSVMVITIGOVSGSLGTDAFQEVDFGLTLPY 135
 QY 119 ----LFKESGCGYCEWVNGSGEGRILLHAIQSTMAKGYSVVVYIPEDIAKEDAGDGTYSN 174
 DB 136 KHSYVVRERK-----EMGRIVAESFFIAKYGRPVLDIPKDVGLEKFDYQIVNP 186
 QY 175 STTS-SGTPVVP-DPTLEAALVEALINNAKSVTLFCGAG--VKNARAQVLELAERIKSPI 230
 DB 187 NNINLACGVKMYDONRISQAANLIKQSSQPLLYTGGAIVNSINNELINLAKIIV 246
 QY 231 GHALGKQYLOHNEPREVNGSGLLGACVDAASNEADLLILGLTF-----PYSPLER 284
 DB 247 ATTLMGKGIIDESHPLSLGMLGHWGTYVANYAVSECDLLIALCARPDDRYTGKIDEFACH 306
 QY 285 DNAQVDINGANHGRRTYKYPRTGVAAATIEHLPHVAKETRSPLDRMLKHEKISS 344
 DB 307 AOYIHVDIDPAETGKRNKTPQIGIVGEIKDFVRLIECL--KNDINFDSEOSQAWRSRIIR 364
 QY 345 VVEYTHNVKRYV-PIHPEVASILNELADR--DAVFTVDTGCMVHARYIENPEGTBD 401
 DB 365 WKREYFLVLPKNNINLSPQ---EVIHEISTEATINAVFTTDVGQHQWMAAQFITSQ--KR 419
 QY 402 FVSGFRHGTMANALPHAQSVDRNRQVIAMCGDGLGLMLGELLTVKLHQLPLKAAVVF 461
 DB 420 WITSAGLGTWGYLPAIPAIGQIAHNPQGVICISDASFQNNIOELGTVSQYGGPIKIFII 479
 QY 462 NNSLSLGMV--LEMLVGCQPFEGTDHEE--VNFALIAAAGIKSVRLTDPKVKVEOLAAL 518
 DB 480 NNRWQGVWQMOAGFYGERYSNMEKGAENFTKVAEAFGLRSKRLKSRNDLRLKEAL 539

QY 519 AYPGVILIDI--VTDPNAL-SIPPTTWEQVGFSS 550
 DB 540 DYDGEILVDIOVYADENCYPMVAVPCKSNAQMGIN 574

RESULT 7
 ID ILVB.PORU STANDARD; PRT; 590 AA.
 AC P31594;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ACETOYLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS)
 DE (ACETOHYDROXY-ACID SYNTHASE LARGE SUBUNIT) (ALS).
 GN ILVB.
 OS Porphyra purpurea, and Porphyra umbilicalis (Laver).
 OG Chloroplast.
 CC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.PURPUREA; STRAIN=AVONPORT;
 RA Reith M.E., Munnholland J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
 genome.";
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.UMBILICALIS; STRAIN=AVONPORT;
 RX MEDLINE=93135832; PubMed=8381336;
 RA Reith M., Munnholland J.M.;
 RT "Two amino-acid biosynthetic genes are encoded on the plastid genome
 of the red alga Porphyra umbilicalis.";
 RT Curr. Genet. 23:59-65(1993).
 CC -1- CATALYTIC ACTIVITY: 2-ACETOYLACTATE + CO(2) = 2-PYRUVATE.
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION
 CC (BY SIMILARITY).
 CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
 CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY).
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
 CC -----
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 CC -----
 DR EMBL: U38804; AAC08216.1; -
 DR EMBL: M94625; AAA03052.1; -
 DR PIR: S27402; S27402.
 DR PIR: S28920; S28920.
 DR HSP: P06169; 1YPD.
 DR INTERPRO: IPR000399; -
 DR PFAM: PF00205; TPP_ENZYMES; 1.
 DR PROSITE: PS00187; TPP_ENZYMES; 1.
 KW branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;
 KM Thiamine pyrophosphate; Lyase; Chloroplast.
 FT ACT SITE 61 BY SIMILARITY.
 SQ SEQUENCE 590 AA: 64929 MW: 1C35F7DF0F2E57AD CRC64;

Query Match 17.9%; Score 533.5; DB 1; Length 590;
 Best Local Similarity 27.8%; Pred. No. 9,4e-28;
 Matches 161; Conservative 107; Mismatches 256; Indels 55; Gaps 14;

QY 9 LIDTLEAGVKKRYGLVGSUNPIYDAV-----RQSDIEVHVRNEAFAAGASGLING 64
 DB 17 LIDSLVRHCVKKEIFEGYGGALIPYDELAYAMEELSLIKNMLVNRHGGASHADAVSRSTG 76
 QY 65 ELAVCAASGPGNTHLIOGLYDSHRNGAKVLAISHIPSAOIGSTPFQETHPEILFKES 124


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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-85242084; PubMed-2989782;
RA Mek R.C., Hauser G.A., Hatfield G.W.;
RT "The nucleotide sequence of the ilvB operon of Escherichia coli:
RL sequence homologues of the acetylhydroxy acid synthase isozymes.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-85242083; PubMed-2989781;
RA Friden P., Donegan J., Mullen J., Tsui P., Freundlich M.;
RT "The ilvB locus of Escherichia coli K-12 is an operon encoding both
RL subunits of acetylhydroxyacid synthase I.";
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655; PubMed-7686882;
RA Burland V.D., Plunkett G., III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RL genome: organizational symmetry around the origin of replication.";
CC -1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS
CC ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXYBUTANOATE).
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS.
CC -1- MISCELLANEOUS: E.COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN,
CC ILVGM AND ILVH.
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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CC -----
DR EMBL: J01633; AAA24017.1; -
DR EMBL: X02541; AAA26387.1; -
DR EMBL: L10328; AAA62023.1; -
DR EMBL: AE000444; AAC76694.1; -
DR PIR: A23803; YCECIL.
DR SWISS-2DPAGE: P08142; COLI.
DR ECODBASE: D057.0; 6TH EDITION.
DR ECOGENE: B610494; ILVB.
DR INTERPRO: IPR000399; -
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; 1.
KW Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;
KW Thiamine pyrophosphate; Lyase
FT ACT_SITE 60 BY SIMILARITY.
SQ SEQUENCE 562 AA; 60440 MW; 70F8A31280315353C CRC64;

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Query Match 17.5%; Score 523.5; DB 1; Length 562;
Best Local Similarity 27.9%; Pred. No. 4e-27;
Matches 162; Conservative 108; Mismatches 239; Indels 71; Gaps 17;

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DB 196 FSEESI-----RDAAAM--INAAKRPVLYLGGVINAPAVRBLAEKAOLEPTT 241
QY 232 HALGCKOYIENPEFEGMSGILGYCAVSAENADLLILGLTDF-----PVSDFPKD 285
DB 242 MTLNALGMLPRAPLISGMGMHGVSTNYILOADLLIYAGFEDRAIGKEQFCFPA 301
QY 286 NVAQVDINGAHIGRTTVKYP--VTGDVAATTENILPHYEKTDRSFELDMKAHERK- 341
DB 302 KIIVHVDIRALGK---IKOPHVALQADVDDVLAQLIPLV-EAQPRAEWHQVADLQREF 357
QY 342 ---LSVVEYTHNVEKHPVPIHPEYASINELA---DKDAVFTVDTGMCNWHAR--I 393
DB 358 PCPIPKACDPLSH-----YGLINVAACVDNNAITTTDVGQHMTAQAAPL 404
QY 394 ENPESTRDFVSGFRHGTMANALPHALGAOSVDRROYIANOCGGLMLLIGELTLVKHQ 453
DB 405 NRP---RQMLTSGGLTGMFGFLPAIGALANPDKVLCSTGDSLMNTOENATASENQ 461
QY 454 LPLKAVFNNSISLGV-KLEMLVEGOPEFTDHE-EVNFAEIATAAGIKSVRTDPKVR 511
DB 462 LDVKTILLNNALGIVHQOQSLFYEQGVFAATYFGKINFMQIAAGFGLCTDLNNEADPQ 521
QY 512 EQLAEALVPCPVLLIDVTPNAL----SIPTWEQVYG 548
DB 522 ASLQEIINRPGPALIHVRIDAEKRYVMPVPPGAANTEWVG 561

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RESULT 10
ILVB_SPIPL STANDARD; PRT; 579 AA.
ID ILVB_SPIPL
AC P27868;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACETOLACTATE SYNTHASE (EC 4.1.3.18) (ACETOHYDROXY-ACID SYNTHASE) (ALS)
DE (FRAGMENT).
GN ILVY.
OS *Spirulina platensis*.
OC Bacteria; Cyanobacteria; Oscillatoriales; *Spirulina*.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-923814877; PubMed-1512571;
RA Milano A., de Rossi E., Zanaria E., Barbierato L., Ciferri O.,
RA Riccardi G.;
RT "Molecular characterization of the genes encoding acetylhydroxy acid
RT synthase in the cyanobacterium *Spirulina platensis*.";
RL J. Gen. Microbiol. 138:1399-1408(1992).
CC -1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2 PYRUVATE.
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
CC -----
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CC -----
DR EMBL: M75907; AAA26595.1; -
DR PIR: B44857; B44857.
DR HSPD: P06169; IYPD.
DR INTERPRO: IPR000399; -
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; PARTIAL.
KW Branched-chain amino acid biosynthesis; Flavoprotein; Lyase;
KW Thiamine pyrophosphate.
FT ACT_SITE 61 BY SIMILARITY.
FT NON_TER 579
SQ SEQUENCE 579 AA; 63440 MW; BC94FEA728A7889A CRC64;

DR PROSITE: PS00187; TPP_ENZYMES; 1.
 KM Oxidoreductase; Flavoprotein; FAD; Thiamine pyrophosphate; Magnesium.
 FT DOMAIN 1 188 CORE.
 FT DOMAIN 189 336 FAD.
 FT DOMAIN 337 591 TPP.
 FT ACT_SITE 53 53 BY SIMILARITY.
 FT METAL 441 441 MAGNESIUM (BY SIMILARITY).
 FT METAL 468 468 MAGNESIUM (BY SIMILARITY).
 FT METAL 470 470 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 591 AA: 65128 MW: C02462214138635F CRC64;

Query Match 16.5%; Score 492; DB 1; Length 591;
 Best Local Similarity 27.2%; Pred. No. 4.9e-25;
 Matches 146; Conservative 110; Mismatches 230; Indels 50; Gaps 13;

QY 9 LIDTLEAGVKRIYGLVGDSLNPIDYAVRQ-SDIEVHVHNEEAAFAAGASLITGELA 67
 DB 12 MNVLTQWGVDPITYGIPSGTSLSLMDALMEDDIRLOVHEETGALAAVMQAKFEGSIG 71
 QY 68 VCAASGPGNTHLIOGLYDSHNRGAKVLAISHIPSAQISFFQETHPEILFEKCSGYC 127
 DB 72 VAVSGSGPETHLINCIVYDAAMDNPFLAILGSRPNEINMADFELNPNMNGIAYVN 131
 QY 128 EMVNGEGEERILHHAIOSTMAGKGVVVPDIAKEDA-----GDGTYSNSTISGCT 181
 DB 132 KRAVAVEOLPKVIEDACRAAISKKGPAAVEIPVNFGEIDENSYGSGSYERSFTIA--- 188
 QY 182 PVVFPPTFAALVEAINNAKSVTLFCGAGVKNARQVLELAERIKSPIGHALGKQYTO 241
 DB 189 PAL-NEVEIDRAVELLNNAERPVYIAGFGVAKAGEVITELSKIKAPT--ITTGKNFEA 244
 QY 242 HENPFVNGSG--LIGYACVDASNEADLLILGTDFPYSD---FLPKDNVAQVDING 294
 DB 245 FENNYE-GLTGSYKRYGKWRPANEVFEADTVLELGSNFAFAEYKFKTEFIQVDIDP 303
 QY 295 AHIGRTTVKYPVGTGVAATIENTILPHYKE-----KTRSFILDMKAKHERKLS 343
 DB 304 YKLGKRALDASILDGAGAAKILDKVNPVESTPMWRANVKNQNWRYMNL-EGKTE 362
 QY 344 SVYETTHVNEKHPRIHPEYVASILNELDKDAVFVDIGMKNVIAKRIE-NPESTRPE 402
 DB 363 GELQLT-----QVYNAINKHAADODAIYSLDVGSTTQTSRHLHMTPKM--W 407
 QY 403 VGSFRRGTMANALPHAIGASVDNRQVITAMCGDGLGMLGELLTVKJHOLPLKAVEN 462
 DB 408 RISPPLFATGIALPGSLAAKKTDPKQVNNIMDGAFFMNCYPRVITNVQYDLPIVNLVS 467
 QY 463 NSSLGWKLEMLVEGQPEFGTDEEYVFAELIAAAGIKSVRTTPKRVREOLAAL 518
 DB 468 NMEYGRFKKKYEDTNKHLFGVDPETNADYGIKIAEGAVGFTVDRIIDIDAVVAEAV 523

RESULT 15
 ID ILVL_BRNA STANDARD; PRT; 655 AA.
 AC P27818;
 DT 01-AUG-1992 (Rel. 23. Created)
 DT 01-AUG-1992 (Rel. 23. Last sequence update)
 DT 01-OCT-1996 (Rel. 34. Last annotation update)
 DE ACETOYLACTATE SYNTHASE I PRECURSOR (EC 4.1.3.18) (ACETOHYDROXY-ACID
 DE SYNTHASE 1) (ALS 1).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Brassica.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. TOPAS;
 RX MEDLINE=91375448; PubMed=1696019;
 RA Rutledge R.G., Ouellet T., Hattori J., Miki B.L.;
 RT "Molecular characterization and genetic origin of the Brassica napus
 acetohydroxyacid synthase multigene family";

RL Mol. Genet. 229:31-40(1991).
 CC -1- CATALYTIC ACTIVITY: 2-ACETOYLACTATE + CO(2) = 2-PYRUVATE (THIS
 CC ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXY-BUTANOATE).
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
 CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
 CC -1- MISCELLANEOUS: ACETOYLACTATE SYNTHASE IS THE TARGET ENZYME FOR
 CC SULFOXYUREA AND IMIDAZOLINONE HERBICIDES.
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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DR EMBL; Z11524; CAAT7613.1; -.
 DR PIR; S17691; S17691.
 DR HSRP; P06169; 1YPD.
 DR INTERPRO: IPR000399; -.
 DR PFAM: PF00205; TPP_ENZYMES; 1.
 DR PROSITE; PS00187; TPP_ENZYMES; 1.
 KM Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;
 KM Thiamine pyrophosphate; Herbicide resistance; Transit peptide;
 KM Lyase; Chloroplast; Multigene family.
 FT TRANSIT 1 82 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 83 655 ACETOYLACTATE SYNTHASE I.
 FT ACT_SITE 129 129 BY SIMILARITY.
 SQ SEQUENCE 655 AA: 71288 MW: 1B6AD7D7A0DAD91A CRC64;

Query Match 16.1%; Score 480; DB 1; Length 655;
 Best Local Similarity 26.3%; Pred. No. 3.5e-24;
 Matches 149; Conservative 104; Mismatches 269; Indels 44; Gaps 12;

QY 6 ABOLIDTLEAGVKRIYGLVGDSLNPIDYAV-ROSDIEVHVHNEEAAFAAGASLITG 64
 DB 11 LIDTLEAGVKRIYGLVGDSLNPIDYAV-ROSDIEVHVHNEEAAFAAGASLITG 64
 QY 85 ADLVEALEERQGVETFFAVFGAGSMELIHQALTRSTINVLPRHROGGVFAAEGYARRSS 144
 DB 65 ELAVCAASGPGNTHLIOGLYDSHNRGAKVLAISHIPSAQISFFQETHPEILFEKCS 124
 QY 145 KPGICLAISGPATNLVSLDAMLDVPLVAITGOVPRMIGTAPETPIVEYTRST 204
 DB 125 GYCVENNGEGEERILHHAIOSTMAGK-GVSVVVPDIAKEDAGDGYNSNTISGTPV 183
 QY 205 KINYLVMVDLIPRIQVEFFLATGSRGPVLDVYPKDI-QQOLAIPMWDQPMRLPGYMS 263
 DB 184 VEPDPTFAAL--VEAINNAKSVTLFCGAGVKNARQVLELAERIKSPIGHALGKQYI 240
 QY 264 RLPQPPREVSQLQIVALLISESKRPVLYVGSGSLNSSEELGREVELTGIPVASTLGLGSY 323
 QY 241 QHENPFVNGSGLLGYACVDASNEADLLILGTDF-----PYSDFLPKDNVAQVDING 294
 DB 324 PCNDELISQIMGHGTGVYANVAVHSDLLAFGVPRDRTGKLEAFASRAKIVHIDIDS 383
 QY 295 AHIGRTTVKYPVGTGVAATIENTILPHYKEKTRSFILDMKAKHERKLSVETTY 349
 DB 384 AELGKNTKTPHVSVCQDKYALOGMKNVLENRADELKLDGQVARSLSDEKQKFFLSFTTF 443
 QY 350 THNVEKHPRIHPEYVASILNELDKDAVFVDIGMKNVIAKRIE-NPESTRPE 402
 DB 444 GE-----AIPQYAIQLIDELTEKALISTGVGHQWMAAFYKRYK-PRQMLSSSLG 496
 QY 410 TMANLPHAIQASVDNRQVITAMCGDGLGMLGELLTVKJHOLPLKAVENNSSLGW 469
 DB 497 AMGFGLPAAIGASVANPDIVDDGSEFINNVDELATIRENLPVILILNNHILNV 556
 QY 470 KLEMLVEGQPE-----GTDHEE-----VNFAELIAAAGIKSVRTTPKRVREOLA 515
 DB 557 -----MOMEDRFTYKANRAITTYIGDPAARENEITPNMLQFAGAGCIYAANYTKKEELREALQ 611
 QY 516 EALAVPGVPLIDIVDPNALISIPPTI 541

DB 612 TMLDTPGVLDDVIC-PHOENVLPMI 636

Search completed: March 17, 2001, 21:58:58
Job time: 394 sec

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